

1
SEQUENCE LISTING



<110> Hageman, Gregory S.
Kuehn, Markus H.

<120> THERAPEUTICS AND DIAGNOSTICS FOR OCULAR DISEASE BASED
ON A NOVEL HUMAN GENE FAMILY

<130> UIA-027.01

<140> 09/183,972

<141> 1998-10-29

<160> 49

<170> PatentIn Ver. 2.0

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<212> DNA

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<221> CDS

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Glu Ala Val Trp Glu Ala Tyr Arg	Ile Phe Leu Asp Arg Ile Pro Asp	
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aca ggg gaa tat cag gac tgg gtc	agc ttc tgc cag cag gag acc ttc	192
Thr Gly Glu Tyr Gln Asp Trp Val	Ser Phe Cys Gln Gln Glu Thr Phe	
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Cys Leu Phe Asp Ile Gly Gln Asn Phe	Ser Asn Ser Gln Glu His Leu	
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gat ctt ctc cag cag aga ata aaa	cag aga agt ttc cct gag aga aaa	288
Asp Leu Leu Gln Gln Arg Ile Lys	Gln Arg Ser Phe Pro Glu Arg Lys	
85 90	95	
gat gaa gta tct aca gag aag aca	ttg gga gag cct agt gaa acc att	336
Asp Glu Val Ser Thr Glu Lys Thr	Leu Gly Glu Pro Ser Glu Thr Ile	
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gtg gtt tca aca gat gtt gcc agc	gtc tca ctt ggg cct ttc cct gtc	384
Val Val Ser Thr Asp Val Ala Ser	Val Ser Leu Gly Pro Phe Pro Val	
115 120	125	

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gag gag cag agg gtg gag ctc agc atc tct ctg ata aac cag agg ttc 528
 Glu Glu Gln Arg Val Glu Leu Ser Ile Ser Leu Ile Asn Gln Arg Phe
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Thr Gly Glu Tyr Gln Asp Trp Val Ser Phe Cys Gln Gln Glu Thr Phe
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Cys Leu Phe Asp Ile Gly Gln Asn Phe Ser Asn Ser Gln Glu His Leu
 65 70 75 80

Asp Leu Leu Gln Gln Arg Ile Lys Gln Arg Ser Phe Pro Glu Arg Lys
 85 90 95

Asp Glu Val Ser Thr Glu Lys Thr Leu Gly Glu Pro Ser Glu Thr Ile
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Val Val Ser Thr Asp Val Ala Ser Val Ser Leu Gly Pro Phe Pro Val
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Thr Pro Asp Asp Thr Leu Leu Asn Glu Ile Leu Asp Asn Ala Leu Asn
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Asp Thr Lys Met Pro Thr Thr Glu Arg Glu Thr Glu Leu Ala Val Ser
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agccaga atg tat ttg gaa act aga aga gct att ttt gtt ttt tgg att 169
Met Tyr Leu Glu Thr Arg Arg Ala Ile Phe Val Phe Trp Ile
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Phe Leu Gln Val Gln Gly Thr Lys Asp Ile Ser Ile Asn Ile Tyr His
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tct gaa act aaa gac ata gac aat ccc cca aga aat gaa aca act gaa 265
Ser Glu Thr Lys Asp Ile Asp Asn Pro Pro Arg Asn Glu Thr Thr Glu
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agt act gaa aaa atg tac aaa atg tca act atg aga cga ata ttc gat 313
Ser Thr Glu Lys Met Tyr Lys Met Ser Thr Met Arg Arg Ile Phe Asp
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Leu Ala Lys His Arg Thr Lys Arg Ser Ala Phe Phe Pro Thr Gly Val
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aaa gtc tgt cca cag gaa tcc atg aaa cag att tta gac agt ctt caa 409
Lys Val Cys Pro Gln Glu Ser Met Lys Gln Ile Leu Asp Ser Leu Gln
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Ala Tyr Tyr Arg Leu Arg Val Cys Gln Glu Ala Val Trp Glu Ala Tyr
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Val Ser Ile Cys Gln Gln Glu Thr Phe Cys Leu Phe Asp Ile Gly Lys
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Thr	Leu	Gly	Glu	Pro	Gly	Glu	Thr	Ile	Val	Ile	Ser	Thr	Asp	Val	Ala	
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Asn	Val	Ser	Leu	Gly	Pro	Phe	Pro	Leu	Thr	Pro	Asp	Asp	Thr	Leu	Leu	
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Glu	Arg	Glu	Thr	Glu	Phe	Ala	Val	Leu	Glu	Glu	Gln	Arg	Val	Glu	Leu	
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Ser	Val	Ser	Leu	Val	Asn	Gln	Lys	Phe	Lys	Ala	Glu	Leu	Ala	Asp	Ser	
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Gln	Ser	Pro	Tyr	Tyr	Gln	Glu	Leu	Ala	Gly	Lys	Ser	Gln	Leu	Gln	Met	
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Gln	Leu	Thr	Ala	Ile	Phe	Lys	Arg	His	Ser	Ala	Glu	Ala	Lys	Ser	Pro	
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Ala	Ser	Asp	Leu	Leu	Ser	Phe	Asp	Ser	Asn	Lys	Ile	Glu	Ser	Glu	Glu	
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gtc	tat	cat	gga	acc	atg	gag	gag	gac	aag	caa	cca	gaa	atc	tat	ctc	1177
Val	Tyr	His	Gly	Thr	Met	Glu	Glu	Asp	Lys	Gln	Pro	Glu	Ile	Tyr	Leu	
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Ala	Pro	Pro	Phe	Phe	Met	Ala	Ser	Ser	Ile	Phe	Ser	Leu	Thr	Asp	Gln	
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Gly	Thr	Thr	Asp	Thr	Met	Ala	Thr	Asp	Gln	Thr	Met	Leu	Val	Pro	Gly	
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Leu Glu Ile Leu Asn Phe Arg Asn Gly Ser Val Ile Val Asn Ser Lys	
625 630 635	
atg aag ttt gct aag tct gtg ccg tat aac ctc acc aag gct gtg cac	2089
Met Lys Phe Ala Lys Ser Val Pro Tyr Asn Leu Thr Lys Ala Val His	
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655 660 665 670	
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ccc tgc aag ttc ctg gcc tgc ggc gaa ttt gcc caa tgt gta aag aac	2233
Pro Cys Lys Phe Leu Ala Cys Gly Glu Phe Ala Gln Cys Val Lys Asn	
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Glu Arg Thr Glu Glu Ala Glu Cys Arg Cys Lys Pro Gly Tyr Asp Ser	
705 710 715	
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Gln Gly Ser Leu Asp Gly Leu Glu Pro Gly Leu Cys Gly Leu Ala Gln	
720 725 730	
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Arg Asn Ala Arg Ser Ser Arg Glu Arg Glu Leu His Ala Val Pro Asp	
735 740 745 750	
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755 760 765	
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Asn Lys Ile Thr Arg	
770	
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 Glu Lys Met Tyr Lys Met Ser Thr Met Arg Arg Ile Phe Asp Leu Ala
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 Lys His Arg Thr Lys Arg Ser Ala Phe Phe Pro Thr Gly Val Lys Val
 65 70 75 80
 Cys Pro Gln Glu Ser Met Lys Gln Ile Leu Asp Ser Leu Gln Ala Tyr
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 Tyr Arg Leu Arg Val Cys Gln Glu Ala Val Trp Glu Ala Tyr Arg Ile
 100 105 110
 Phe Leu Asp Arg Ile Pro Asp Thr Gly Glu Tyr Gln Asp Trp Val Ser
 115 120 125
 Ile Cys Gln Gln Glu Thr Phe Cys Leu Phe Asp Ile Gly Lys Asn Phe
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 Ser Asn Ser Gln Glu His Leu Asp Leu Leu Gln Gln Arg Ile Lys Gln
 145 150 155 160
 Arg Ser Phe Pro Asp Arg Lys Asp Glu Ile Ser Ala Glu Lys Thr Leu
 165 170 175
 Gly Glu Pro Gly Glu Thr Ile Val Ile Ser Thr Asp Val Ala Asn Val
 180 185 190

Ser	Leu	Gly	Pro	Phe	Pro	Leu	Thr	Pro	Asp	Asp	Thr	Leu	Leu	Asn	Glu	195	200	205	
Ile	Leu	Asp	Asn	Thr	Leu	Asn	Asp	Thr	Lys	Met	Pro	Thr	Thr	Glu	Arg	210	215	220	
Glu	Thr	Glu	Phe	Ala	Val	Leu	Glu	Glu	Gln	Arg	Val	Glu	Leu	Ser	Val	225	230	235	240
Ser	Leu	Val	Asn	Gln	Lys	Phe	Lys	Ala	Glu	Leu	Ala	Asp	Ser	Gln	Ser	245	250	255	
Pro	Tyr	Tyr	Gln	Glu	Leu	Ala	Gly	Lys	Ser	Gln	Leu	Gln	Met	Gln	Lys	260	265	270	
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Arg	Pro	Lys	Lys	Glu	Lys	Asp	Gly	Ser	Ser	Ser	Thr	Glu	Met	Gln	Leu	290	295	300	
Thr	Ala	Ile	Phe	Lys	Arg	His	Ser	Ala	Glu	Ala	Lys	Ser	Pro	Ala	Ser	305	310	315	320
Asp	Leu	Leu	Ser	Phe	Asp	Ser	Asn	Lys	Ile	Glu	Ser	Glu	Glu	Val	Tyr	325	330	335	
His	Gly	Thr	Met	Glu	Glu	Asp	Lys	Gln	Pro	Glu	Ile	Tyr	Leu	Thr	Ala	340	345	350	
Thr	Asp	Leu	Lys	Arg	Leu	Ile	Ser	Lys	Ala	Leu	Glu	Glu	Glu	Gln	Ser	355	360	365	
Leu	Asp	Val	Gly	Thr	Ile	Gln	Phe	Thr	Asp	Glu	Ile	Ala	Gly	Ser	Leu	370	375	380	
Pro	Ala	Phe	Gly	Pro	Asp	Thr	Gln	Ser	Glu	Leu	Pro	Thr	Ser	Phe	Ala	385	390	395	400
Val	Ile	Thr	Glu	Asp	Ala	Thr	Leu	Ser	Pro	Glu	Leu	Pro	Pro	Val	Glu	405	410	415	
Pro	Gln	Leu	Glu	Thr	Val	Asp	Gly	Ala	Glu	His	Gly	Leu	Pro	Asp	Thr	420	425	430	
Ser	Trp	Ser	Pro	Pro	Ala	Met	Ala	Ser	Thr	Ser	Leu	Ser	Glu	Ala	Pro	435	440	445	
Pro	Phe	Phe	Met	Ala	Ser	Ser	Ile	Phe	Ser	Leu	Thr	Asp	Gln	Gly	Thr	450	455	460	
Thr	Asp	Thr	Met	Ala	Thr	Asp	Gln	Thr	Met	Leu	Val	Pro	Gly	Leu	Thr	465	470	475	480
Ile	Pro	Thr	Ser	Asp	Tyr	Ser	Ala	Ile	Ser	Gln	Leu	Ala	Leu	Gly	Ile	485	490	495	

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 515 520 525
 Ala Pro Ser Glu Val Pro Glu Leu Ser Glu Tyr Val Ser Val Pro Asp
 530 535 540
 His Phe Leu Glu Asp Thr Thr Pro Val Ser Ala Leu Gln Tyr Ile Thr
 545 550 555 560
 Thr Ser Ser Met Thr Ile Ala Pro Lys Gly Arg Glu Leu Val Val Phe
 565 570 575
 Phe Ser Leu Arg Val Ala Asn Met Ala Phe Ser Asn Asp Leu Phe Asn
 580 585 590
 Lys Ser Ser Leu Glu Tyr Arg Ala Leu Glu Gln Gln Phe Thr Gln Leu
 595 600 605
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 610 615 620
 Ile Leu Asn Phe Arg Asn Gly Ser Val Ile Val Asn Ser Lys Met Lys
 625 630 635 640
 Phe Ala Lys Ser Val Pro Tyr Asn Leu Thr Lys Ala Val His Gly Val
 645 650 655
 Leu Glu Asp Phe Arg Ser Ala Ala Ala Gln Gln Leu His Leu Glu Ile
 660 665 670
 Asp Ser Tyr Ser Leu Asn Ile Glu Pro Ala Asp Gln Ala Asp Pro Cys
 675 680 685
 Lys Phe Leu Ala Cys Gly Glu Phe Ala Gln Cys Val Lys Asn Glu Arg
 690 695 700
 Thr Glu Glu Ala Glu Cys Arg Cys Lys Pro Gly Tyr Asp Ser Gln Gly
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 Ser Leu Asp Gly Leu Glu Pro Gly Leu Cys Gly Leu Ala Gln Arg Asn
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tggaagtttc aaggatttgg acactcaatt aaggattctg tctctctctc attcctttgg 180

ttttggccca a atg att atg ttt cct ctt ttt ggg aag att tct ctg ggt 230

Met Ile Met Phe Pro Leu Phe Gly Lys Ile Ser Leu Gly
1 5 10

att ttg ata ttt gtc ctg ata gaa gga gac ttt cea tca tta aca gca 278

Ile Leu Ile Phe Val Leu Ile Glu Gly Asp Phe Pro Ser Leu Thr Ala
15 20 25

caa acc tac tta tct ata gag gag atc caa gaa ccc aag agt gca gtt 326

Gln Thr Tyr Leu Ser Ile Glu Glu Ile Gln Glu Pro Lys Ser Ala Val
30 35 40 45

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Ser Phe Leu Leu Pro Glu Glu Ser Thr Asp Leu Ser Leu Ala Thr Lys
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Lys Lys Gln Pro Leu Asp Arg Arg Glu Thr Glu Arg Gln Trp Leu Ile
65 70 75

aga agg cgg aga tct att ctg ttt cct aat gga gtg aaa atc tgc cca 470

Arg Arg Arg Arg Ser Ile Leu Phe Pro Asn Gly Val Lys Ile Cys Pro
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gat gaa agt gtt gca gag gct gtg gca aat cat gtg aag tat ttt aaa 518

Asp Glu Ser Val Ala Glu Ala Val Ala Asn His Val Lys Tyr Phe Lys
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gtc cga gtg tgt cag gaa gct gtc tgg gaa gcc ttc agg act ttt tgg 566

Val Arg Val Cys Gln Glu Ala Val Trp Glu Ala Phe Arg Thr Phe Trp
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gat cga ctt cct ggg cgt gag gaa tat cat tac tgg atg aat ttg tgt 614

Asp Arg Leu Pro Gly Arg Glu Glu Tyr His Tyr Trp Met Asn Leu Cys
130 135 140

gag gat gga gtc aca agt ata ttt gaa atg ggc aca aat ttt agt gaa 662

Glu Asp Gly Val Thr Ser Ile Phe Glu Met Gly Thr Asn Phe Ser Glu
145 150 155

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Ser	Val	Glu	His	Arg	Ser	Leu	Ile	Met	Lys	Lys	Leu	Thr	Tyr	Ala	Lys	
		160					165					170				
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Glu	Thr	Val	Ser	Ser	Ser	Glu	Leu	Ser	Ser	Pro	Val	Pro	Val	Gly	Asp	
	175					180					185					
act	tca	aca	ttg	gga	gac	act	act	ctc	agt	gtt	cca	cat	cca	gag	gtg	806
Thr	Ser	Thr	Leu	Gly	Asp	Thr	Thr	Leu	Ser	Val	Pro	His	Pro	Glu	Val	
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gac	gcc	tat	gaa	ggg	gcc	tca	gag	agc	agc	ttg	gaa	agg	cca	gag	gag	854
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agt	att	agc	aat	gaa	att	gag	aat	gtg	ata	gaa	gaa	gcc	aca	aaa	cca	902
Ser	Ile	Ser	Asn	Glu	Ile	Glu	Asn	Val	Ile	Glu	Glu	Ala	Thr	Lys	Pro	
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Tyr	Arg	Glu	Glu	Leu	Gln	Asp	Ser	Ser	Ser	Phe	His	His	Gln	His	Leu	
	255					260					265					
gaa	gaa	gaa	ttt	att	tca	gag	gtt	gaa	aat	gca	ttt	act	ggg	tta	cca	1046
Glu	Glu	Glu	Phe	Ile	Ser	Glu	Val	Glu	Asn	Ala	Phe	Thr	Gly	Leu	Pro	
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ggc	tac	aag	gaa	att	cgt	gta	ctt	gaa	ttt	agg	tcc	ccc	aag	gaa	aat	1094
Gly	Tyr	Lys	Glu	Ile	Arg	Val	Leu	Glu	Phe	Arg	Ser	Pro	Lys	Glu	Asn	
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gac	agt	ggc	gta	gat	gtt	tac	tat	gca	gtt	acc	ttc	aat	ggg	gag	gcc	1142
Asp	Ser	Gly	Val	Asp	Val	Tyr	Tyr	Ala	Val	Thr	Phe	Asn	Gly	Glu	Ala	
			305					310					315			
atc	agc	aat	acc	acc	tgg	gac	ctc	att	agc	ctt	cac	tcc	aac	aag	gtg	1190
Ile	Ser	Asn	Thr	Thr	Trp	Asp	Leu	Ile	Ser	Leu	His	Ser	Asn	Lys	Val	
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Glu	Asn	His	Gly	Leu	Val	Glu	Leu	Asp	Asp	Lys	Pro	Thr	Val	Val	Tyr	
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aca	atc	agt	aac	ttc	aga	gat	tat	att	gct	gag	aca	ttg	cag	cag	aat	1286
Thr	Ile	Ser	Asn	Phe	Arg	Asp	Tyr	Ile	Ala	Glu	Thr	Leu	Gln	Gln	Asn	
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Phe	Leu	Leu	Gly	Asn	Ser	Ser	Leu	Asn	Pro	Asp	Pro	Asp	Ser	Leu	Gln	
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Leu Ile Asn Val Arg Gly Val Leu Arg His Gln Thr Glu Asp Leu Val	
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tgg aac acc caa agt tca agt ctt cag gca acg ccg tca tct att ctg	1430
Trp Asn Thr Gln Ser Ser Ser Leu Gln Ala Thr Pro Ser Ser Ile Leu	
400 405 410	
gat aat acc ttt caa gct gca tgg ccc tca gca gat gaa tcc atc acc	1478
Asp Asn Thr Phe Gln Ala Ala Trp Pro Ser Ala Asp Glu Ser Ile Thr	
415 420 425	
agc agt att cca cca ctt gat ttc agc tct ggt cct ccc tca gcc act	1526
Ser Ser Ile Pro Pro Leu Asp Phe Ser Ser Gly Pro Pro Ser Ala Thr	
430 435 440 445	
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Gly Arg Glu Leu Trp Ser Glu Ser Pro Leu Gly Asp Leu Val Ser Thr	
450 455 460	
cac aaa tta gcc ttt ccc tcg aag atg ggc ctc agc tct tcc cca gag	1622
His Lys Leu Ala Phe Pro Ser Lys Met Gly Leu Ser Ser Ser Pro Glu	
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Val Leu Glu Val Ser Ser Leu Thr Leu His Ser Val Thr Pro Ala Val	
480 485 490	
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Leu Gln Thr Gly Leu Pro Val Ala Ser Glu Glu Arg Thr Ser Gly Ser	
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His Leu Val Glu Asp Gly Leu Ala Asn Val Glu Glu Ser Glu Asp Phe	
510 515 520 525	
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Leu Ser Ile Asp Ser Leu Pro Ser Ser Ser Phe Thr Gln Pro Val Pro	
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Lys Glu Thr Ile Pro Ser Met Glu Asp Ser Asp Val Ser Leu Thr Ser	
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Ser Pro Tyr Leu Thr Ser Ser Ile Pro Phe Gly Leu Asp Ser Leu Thr	
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Ser Lys Val Lys Asp Gln Leu Lys Val Ser Pro Phe Leu Pro Asp Ala	
575 580 585	
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Ser Met Glu Lys Glu Leu Ile Phe Asp Gly Gly Leu Gly Ser Gly Ser	
590 595 600 605	

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Gly	Gln	Lys	Val	Asp	Leu	Ile	Thr	Trp	Pro	Trp	Ser	Glu	Thr	Ser	Ser	
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Glu	Lys	Ser	Ala	Glu	Pro	Leu	Ser	Lys	Pro	Trp	Leu	Glu	Asp	Asp	Asp	
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Ser	Leu	Leu	Pro	Ala	Glu	Ile	Glu	Asp	Lys	Lys	Leu	Val	Leu	Val	Asp	
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aaa	atg	gat	tcc	aca	gac	caa	att	agt	aag	cac	tca	aaa	tat	gaa	cat	2198
Lys	Met	Asp	Ser	Thr	Asp	Gln	Ile	Ser	Lys	His	Ser	Lys	Tyr	Glu	His	
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gct	gtg	ccc	atc	ttc	gca	gat	act	gca	gct	gaa	tct	gcg	tct	cta	acc	2294
Ala	Val	Pro	Ile	Phe	Ala	Asp	Thr	Ala	Ala	Glu	Ser	Ala	Ser	Leu	Thr	
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Leu	Pro	Lys	His	Ile	Ser	Glu	Val	Pro	Gly	Val	Asp	Asp	Cys	Ser	Val	
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Thr	Lys	Ala	Pro	Leu	Ile	Leu	Thr	Ser	Val	Ala	Ile	Ser	Ala	Ser	Thr	
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Asp	Lys	Ser	Asp	Gln	Ala	Asp	Ala	Ile	Leu	Arg	Glu	Asp	Met	Glu	Gln	
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Ile	Thr	Glu	Ser	Ser	Asn	Tyr	Glu	Trp	Phe	Asp	Ser	Glu	Val	Ser	Met	
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Val	Lys	Pro	Asp	Met	Gln	Thr	Leu	Trp	Thr	Ile	Leu	Pro	Glu	Ser	Glu	
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Arg	Val	Trp	Thr	Arg	Thr	Ser	Ser	Leu	Glu	Lys	Leu	Ser	Arg	Asp	Ile	
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Leu	Ala	Ser	Thr	Pro	Gln	Ser	Ala	Asp	Arg	Leu	Trp	Leu	Ser	Val	Thr	
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Gln	Ser	Thr	Lys	Leu	Pro	Pro	Thr	Thr	Ile	Ser	Thr	Leu	Leu	Glu	Asp	
	815					820					825					

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Glu Val Ile Met Gly Val Gln Asp Ile Ser Leu Glu Leu Asp Arg Ile	
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ggc aca gat tac tat cag cct gag caa gtc caa gag caa aat ggc aag	2774
Gly Thr Asp Tyr Tyr Gln Pro Glu Gln Val Gln Glu Gln Asn Gly Lys	
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Val Gly Ser Tyr Val Glu Met Ser Thr Ser Val His Ser Thr Glu Met	
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Val Ser Val Ala Trp Pro Thr Glu Gly Gly Asp Asp Leu Ser Tyr Thr	
880 885 890	
cag act tca gga gct ttg gtg gtt ttc ttc agc ctc cga gtg act aac	2918
Gln Thr Ser Gly Ala Leu Val Val Phe Phe Ser Leu Arg Val Thr Asn	
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Met Met Phe Ser Glu Asp Leu Phe Asn Lys Asn Ser Leu Glu Tyr Lys	
910 915 920 925	
gcc ctg gag caa aga ttc tta gaa ttg ctg gtt ccc tat ctc cag tca	3014
Ala Leu Glu Gln Arg Phe Leu Glu Leu Leu Val Pro Tyr Leu Gln Ser	
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Asn Leu Thr Gly Phe Gln Asn Leu Glu Ile Leu Asn Phe Arg Asn Gly	
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Ser Ile Val Val Asn Ser Arg Met Lys Phe Ala Asn Ser Val Pro Pro	
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aac gtc aac aat gcg gtg tac atg att ctg gaa gac ttt tgt acc act	3158
Asn Val Asn Asn Ala Val Tyr Met Ile Leu Glu Asp Phe Cys Thr Thr	
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Cys Phe Pro Gly Tyr Leu Ser Val Glu Glu Arg Pro Cys Gln Ser Leu	
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 Trp Tyr Arg Gly Lys His Cys Glu Glu Phe Val Ser Glu Pro Val Ile
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 Ile Gly Ile Thr Ile Ala Ser Val Val Gly Leu Leu Val Ile Phe Ser
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 Ala Ile Ile Tyr Phe Phe Ile Arg Thr Leu Gln Ala His His Asp Arg
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 Val Ala Glu Ala Val Ala Asn His Val Lys Tyr Phe Lys Val Arg Val
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 Cys Gln Glu Ala Val Trp Glu Ala Phe Arg Thr Phe Trp Asp Arg Leu
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 Pro Gly Arg Glu Glu Tyr His Tyr Trp Met Asn Leu Cys Glu Asp Gly
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 Val Thr Ser Ile Phe Glu Met Gly Thr Asn Phe Ser Glu Ser Val Glu
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 His Arg Ser Leu Ile Met Lys Lys Leu Thr Tyr Ala Lys Glu Thr Val
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 Ser Ser Ser Glu Leu Ser Ser Pro Val Pro Val Gly Asp Thr Ser Thr
 180 185 190
 Leu Gly Asp Thr Thr Leu Ser Val Pro His Pro Glu Val Asp Ala Tyr
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 Asn Glu Ile Glu Asn Val Ile Glu Glu Ala Thr Lys Pro Ala Gly Glu
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 Gln Ile Ala Glu Phe Ser Ile His Leu Leu Gly Lys Gln Tyr Arg Glu
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Pro	Pro	Leu	Asp	Phe	Ser	Ser	Gly	Pro	Pro	Ser	Ala	Thr	Gly	Arg	Glu	
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Pro	Ala	Glu	Ile	Glu	Asp	Lys	Lys	Leu	Val	Leu	Val	Asp	Lys	Met	Asp
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Ser	Thr	Asp	Gln	Ile	Ser	Lys	His	Ser	Lys	Tyr	Glu	His	Asp	Asp	Arg
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Pro	Leu	Ile	Leu	Thr	Ser	Val	Ala	Ile	Ser	Ala	Ser	Thr	Asp	Lys	Ser
			725						730					735	
Asp	Gln	Ala	Asp	Ala	Ile	Leu	Arg	Glu	Asp	Met	Glu	Gln	Ile	Thr	Glu
		740						745					750		
Ser	Ser	Asn	Tyr	Glu	Trp	Phe	Asp	Ser	Glu	Val	Ser	Met	Val	Lys	Pro
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Asp	Met	Gln	Thr	Leu	Trp	Thr	Ile	Leu	Pro	Glu	Ser	Glu	Arg	Val	Trp
	770					775						780			
Thr	Arg	Thr	Ser	Ser	Leu	Glu	Lys	Leu	Ser	Arg	Asp	Ile	Leu	Ala	Ser
	785				790					795					800
Thr	Pro	Gln	Ser	Ala	Asp	Arg	Leu	Trp	Leu	Ser	Val	Thr	Gln	Ser	Thr
			805						810					815	
Lys	Leu	Pro	Pro	Thr	Thr	Ile	Ser	Thr	Leu	Leu	Glu	Asp	Glu	Val	Ile
		820						825					830		
Met	Gly	Val	Gln	Asp	Ile	Ser	Leu	Glu	Leu	Asp	Arg	Ile	Gly	Thr	Asp
		835					840					845			
Tyr	Tyr	Gln	Pro	Glu	Gln	Val	Gln	Glu	Gln	Asn	Gly	Lys	Val	Gly	Ser
	850					855					860				
Tyr	Val	Glu	Met	Ser	Thr	Ser	Val	His	Ser	Thr	Glu	Met	Val	Ser	Val
865					870					875					880

Ala	Trp	Pro	Thr	Glu	Gly	Gly	Asp	Asp	Leu	Ser	Tyr	Thr	Gln	Thr	Ser	885	890	895	
Gly	Ala	Leu	Val	Val	Phe	Phe	Ser	Leu	Arg	Val	Thr	Asn	Met	Met	Phe	900	905	910	
Ser	Glu	Asp	Leu	Phe	Asn	Lys	Asn	Ser	Leu	Glu	Tyr	Lys	Ala	Leu	Glu	915	920	925	
Gln	Arg	Phe	Leu	Glu	Leu	Leu	Val	Pro	Tyr	Leu	Gln	Ser	Asn	Leu	Thr	930	935	940	
Gly	Phe	Gln	Asn	Leu	Glu	Ile	Leu	Asn	Phe	Arg	Asn	Gly	Ser	Ile	Val	945	950	955	960
Val	Asn	Ser	Arg	Met	Lys	Phe	Ala	Asn	Ser	Val	Pro	Pro	Asn	Val	Asn	965	970	975	
Asn	Ala	Val	Tyr	Met	Ile	Leu	Glu	Asp	Phe	Cys	Thr	Thr	Ala	Tyr	Asn	980	985	990	
Thr	Met	Asn	Leu	Ala	Ile	Asp	Lys	Tyr	Ser	Leu	Asp	Val	Glu	Ser	Gly	995	1000	1005	
Asp	Glu	Ala	Asn	Pro	Cys	Lys	Phe	Gln	Ala	Cys	Asn	Glu	Phe	Ser	Glu	1010	1015	1020	
Cys	Leu	Val	Asn	Pro	Trp	Ser	Gly	Glu	Ala	Lys	Cys	Arg	Cys	Phe	Pro	1025	1030	1035	1040
Gly	Tyr	Leu	Ser	Val	Glu	Glu	Arg	Pro	Cys	Gln	Ser	Leu	Cys	Asp	Leu	1045	1050	1055	
Gln	Pro	Asp	Phe	Cys	Leu	Asn	Asp	Gly	Lys	Cys	Asp	Ile	Met	Pro	Gly	1060	1065	1070	
His	Gly	Ala	Ile	Cys	Arg	Cys	Arg	Val	Gly	Glu	Asn	Trp	Trp	Tyr	Arg	1075	1080	1085	
Gly	Lys	His	Cys	Glu	Glu	Phe	Val	Ser	Glu	Pro	Val	Ile	Ile	Gly	Ile	1090	1095	1100	
Thr	Ile	Ala	Ser	Val	Val	Gly	Leu	Leu	Val	Ile	Phe	Ser	Ala	Ile	Ile	1105	1110	1115	1120
Tyr	Phe	Phe	Ile	Arg	Thr	Leu	Gln	Ala	His	His	Asp	Arg	Ser	Glu	Arg	1125	1130	1135	
Glu	Ser	Pro	Phe	Ser	Gly	Ser	Ser	Arg	Gln	Pro	Asp	Ser	Leu	Ser	Ser	1140	1145	1150	
Ile	Glu	Asn	Ala	Val	Lys	Tyr	Asn	Pro	Val	Tyr	Glu	Ser	His	Arg	Ala	1155	1160	1165	
Gly	Cys	Glu	Lys	Tyr	Glu	Gly	Pro	Tyr	Pro	Gln	His	Pro	Phe	Tyr	Ser	1170	1175	1180	

20

Ser Ala Ser Gly Asp Val Ile Gly Gly Leu Ser Arg Glu Glu Ile Arg
185 1190 1195 1200

Gln Met Tyr Glu Ser Ser Glu Leu Ser Arg Glu Glu Ile Gln Glu Arg
1205 1210 1215

Met Arg Val Leu Glu Leu Tyr Ala Asn Asp Pro Glu Phe Ala Ala Phe
1220 1225 1230

Val Arg Glu Gln Gln Val Glu Glu Val
1235 1240

<210> 7
<211> 20
<212> PRT
<213> rattus

<400> 7
Ser Ile Leu Phe Pro Asn Gly Val Arg Ile Cys Pro Ser Asp Thr Val
1 5 10 15

Ala Glu Ala Val
20

<210> 8
<211> 20
<212> PRT
<213> porcine

<220>
<221> UNSURE
<222> (1)..(20)
<223> applicants are unsure of residues designated as
"Xaa" at positions 1 & 11

<400> 8
Xaa Val Phe Phe Pro Thr Gly Val Lys Val Xaa Pro Gln Glu Ser Met
1 5 10 15

Lys Gln Ile Leu
20

<210> 9
<211> 10
<212> PRT
<213> porcine

<220>
<221> UNSURE
<222> (1)..(10)
<223> applicants are unsure of residues designated as
"Xaa" at position 1

<400> 9
 Xaa Val Leu Phe Pro Asn Gly Val Lys Ile
 1 5 10

<210> 10
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<220>
 <221> modified_base
 <222> (25)
 <223> i

<400> 10
 tattaggaat tccatyttyt tyccnaaygg

30

<210> 11
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<220>
 <221> modified_base
 <222> (1)..(26)
 <223> "n" at positions 3, 6, 9 & 24 represent "inosine"

<400> 11
 ttncncgcna gytctgrta rtangg

26

<210> 12
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 12
 ggatttttct ccaagttcaa gg

22

<210> 13
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 13
acgggggtta aagtctgtcc

20

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 14
cgaacaaaaa gatccgcatt

20

<210> 15
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 15
ccttctgcct ctttgacatt g

21

<210> 16
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 16
atcaggactg ggtcagcatc

20

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 17
tcaacagatg ttgccaacgt

20

<210> 18
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 18

gagcctgggtg aaaccattgt

20

<210> 19

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 19

gtggagctca gcgtctctct

20

<210> 20

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 20

tgtgttggag gagcagagg

19

<210> 21

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 21

aaaagatggc tcaagctcca

20

<210> 22

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 22

gaaacttcca ggattcaaaa aa

22

<210> 23

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 23

aggaggacaa gcaaccagaa

20

<210> 24

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 24

tccaacaaaa ttgaaagtga gg

22

<210> 25

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 25

aatcagagct gcccacatct

20

<210> 26

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 26

agccttttgt cctgacacc

19

<210> 27

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 27

ccacctttct ttatggcatc a

21

<210> 28

<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 28
agtgcaggtg gcgaagatat

20

<210> 29
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 29
ctccctgtca gaagctccac

20

<210> 30
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 30
ccacctgcat cttcagatga ca

22

<210> 31
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 31
agttctatga ccattgcccc

20

<210> 32
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 32
aggataccac tcctgtctca gc

22

<210> 33
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 33
aacaattcac acagctgctg g

21

<210> 34
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 34
ccgagctctg gagcaac

17

<210> 35
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 35
gaggattttc gttctgctgc

20

<210> 36
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 36
tctgtgccgt ataacctcac

20

<210> 37
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 37

gactgaggaa gcggagtgtc

20

<210> 38
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 38
acgaacggac tgaggaag

18

<210> 39
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 39
ttctgaatta ctgaccgtag aa

22

<210> 40
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 40
ttccaaaatc aacaaaataa ca

22

<210> 41
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 41
ggtcacaaa atccagacat a

21

<210> 42
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 42
 tgccttctca aggaaaatgg agacagg

27

<210> 43
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 43
 taagccaggt ttgcttccac

20

<210> 44
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 44
 taaaacccca aatgcaatca

20

<210> 45
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 45
 gcaggtctct ctaaacgcat g

21

<210> 46
 <211> 15
 <212> PRT
 <213> Homo sapiens

<220>
 <221> UNSURE
 <222> (1)..(15)
 <223> applicants are unsure of residues designated as
 "Xaa" at positions 1 & 11

<400> 46
 Xaa Ala Leu Phe Pro Asn Gly Val Leu Ile Xaa Pro Xaa Glu Val
 1 5 10 15

<210> 47

<211> 19
 <212> PRT
 <213> Callimico sp.

<220>
 <221> UNSURE
 <222> (1)..(19)
 <223> applicants are unsure of residues designated as
 "Xaa" at positions 1, 11 & 16

<400> 47
 Xaa Ile Leu Phe Pro Asn Gly Val Leu Ile Xaa Pro Asp Glu Val Xaa
 1 5 10 15

Lys Glu Ile

<210> 48
 <211> 20
 <212> PRT
 <213> Homo sapiens

<400> 48
 Ser Ala Phe Phe Pro Thr Gly Val Lys Val Cys Pro Gln Glu Ser Met
 1 5 10 15

Lys Gln Ile Leu
 20

<210> 49
 <211> 18
 <212> PRT
 <213> Callimico sp.

<220>
 <221> UNSURE
 <222> (1)..(18)
 <223> applicants are unsure of residues designated as
 "Xaa" at positions 1 & 11

<400> 49
 Xaa Ile Phe Phe Pro Thr Gly Val Lys Val Xaa Pro Gln Glu Ser Met
 1 5 10 15

Lys Gln